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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/747,521

DATE: 05/10/2001

TIME: 13:02:09

Input Set : A:\227274079.ST25.txt

Output Set: N:\CRF3\05102001\I747521.raw

ENTERED

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3 <110> APPLICANT: Galloway, Darrel
4   Mateczun, Alfred
6 <120> TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
8 <130> FILE REFERENCE: 22727/04079
10 <140> CURRENT APPLICATION NUMBER: 09/747,521
11 <141> CURRENT FILING DATE: 2000-12-21
13 <160> NUMBER OF SEQ ID NOS: 8
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 2430
19 <212> TYPE: DNA
20 <213> ORGANISM: Bacillus anthracis
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23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(2430)
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28 Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu
29 1      5      10      15
31 gta aca gca att act ttg agt ggt ccc gtc ttt atc ccc ctt gta cag      96
32 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln
33      20      25      30
35 ggg gcg ggc ggt cat ggt gat gta ggt atg cac gta aaa gag aaa gag      144
36 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
37      35      40      45
39 aaa aat aaa gat gag aat aag aga aaa gat gaa gaa cga aat aaa aca      192
40 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
41      50      55      60
43 cag gaa gag cat tta aag gaa atc atg aaa cac att gta aaa ata gaa      240
44 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
45 65      70      75      80
47 gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca gaa aag cta ctt      288
48 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
49      85      90      95
51 gag aaa gta cca tct gat gtt tta gag atg tat aaa gca att gga gga      336
52 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly
53      100      105      110
55 aag ata tat att gtg gat ggt gat att aca aaa cat ata tct tta gaa      384
56 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
57      115      120      125
59 gca tta tct gaa gat aag aaa aaa ata aaa gac att tat ggg aaa gat      432
60 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
61      130      135      140
63 gct tta tta cat gaa cat tat gta tat gca aaa gaa gga tat gaa ccc      480
64 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
65 145      150      155      160
67 gta ctt gta atc caa tct tcg gaa gat tat gta gaa aat act gaa aag      528

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68	Val	Leu	Val	Ile	Gln	Ser	Ser	Glu	Asp	Tyr	Val	Glu	Asn	Thr	Glu	Lys	
69					165				170					175			
71	gca	ctg	aac	gtt	tat	tat	gaa	ata	ggg	aag	ata	tta	tca	agg	gat	att	576
72	Ala	Leu	Asn	Val	Tyr	Tyr	Glu	Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile	
73					180				185					190			
75	tta	agt	aaa	att	aat	caa	cca	tat	cag	aaa	ttt	tta	gat	gta	tta	aat	624
76	Leu	Ser	Lys	Ile	Asn	Gln	Pro	Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn	
77			195					200					205				
79	acc	att	aaa	aat	gca	tct	gat	tca	gat	gga	caa	gat	ctt	tta	ttt	act	672
80	Thr	Ile	Lys	Asn	Ala	Ser	Asp	Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr	
81		210					215					220					
83	aat	cag	ctt	aag	gaa	cat	ccc	aca	gac	ttt	tct	gta	gaa	ttc	ttg	gaa	720
84	Asn	Gln	Leu	Lys	Glu	His	Pro	Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu	
85	225					230				235				240			
87	caa	aat	agc	aat	gag	gta	caa	gaa	gta	ttt	gcg	aaa	gct	ttt	gca	tat	768
88	Gln	Asn	Ser	Asn	Glu	Val	Gln	Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr	
89				245					250				255				
91	tat	atc	gag	cca	cag	cat	cgt	gat	gtt	tta	cag	ctt	tat	gca	ccg	gaa	816
92	Tyr	Ile	Glu	Pro	Gln	His	Arg	Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu	
93			260					265				270					
95	gct	ttt	aat	tac	atg	gat	aaa	ttt	aac	gaa	caa	gaa	ata	aat	cta	tcc	864
96	Ala	Phe	Asn	Tyr	Met	Asp	Lys	Phe	Asn	Glu	Gln	Glu	Ile	Asn	Leu	Ser	
97		275					280					285					
99	ttg	gaa	gaa	ctt	aaa	gat	caa	cgg	atg	ctg	tca	aga	tat	gaa	aaa	tgg	912
100	Leu	Glu	Glu	Leu	Lys	Asp	Gln	Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp	
101		290					295					300					
103	gaa	aag	ata	aaa	cag	cac	tat	caa	cac	tgg	agc	gat	tct	tta	tct	gaa	960
104	Glu	Lys	Ile	Lys	Gln	His	Tyr	Gln	His	Trp	Ser	Asp	Ser	Leu	Ser	Glu	
105	305					310				315				320			
107	gaa	gga	aga	gga	ctt	tta	aaa	aag	ctg	cag	att	cct	att	gag	cca	aag	1008
108	Glu	Gly	Arg	Gly	Leu	Lys	Lys	Leu	Gln	Ile	Pro	Ile	Glu	Pro	Lys		
109				325					330				335				
111	aaa	gat	gac	ata	att	cat	tct	tta	tct	caa	gaa	gaa	aaa	gag	ctt	cta	1056
112	Lys	Asp	Asp	Ile	Ile	His	Ser	Leu	Ser	Gln	Glu	Glu	Lys	Glu	Leu	Leu	
113			340					345				350					
115	aaa	aga	ata	caa	att	gat	agt	agt	gat	ttt	tta	tct	act	gag	gaa	aaa	1104
116	Lys	Arg	Ile	Gln	Ile	Asp	Ser	Ser	Asp	Phe	Leu	Ser	Thr	Glu	Glu	Lys	
117			355					360				365					
119	gag	ttt	tta	aaa	aag	cta	caa	att	gat	att	cgt	gat	tct	tta	tct	gaa	1152
120	Glu	Phe	Leu	Lys	Lys	Leu	Gln	Ile	Asp	Ile	Arg	Asp	Ser	Leu	Ser	Glu	
121		370					375					380					
123	gaa	gaa	aaa	gag	ctt	tta	aat	aga	ata	cag	gtg	gat	agt	agt	aat	cct	1200
124	Glu	Glu	Lys	Glu	Leu	Leu	Asn	Arg	Ile	Gln	Val	Asp	Ser	Ser	Asn	Pro	
125	385					390				395				400			
127	tta	tct	gaa	aaa	gaa	aaa	gag	ttt	tta	aaa	aag	ctg	aaa	ctt	gat	att	1248
128	Leu	Ser	Glu	Lys	Glu	Lys	Glu	Phe	Leu	Lys	Lys	Leu	Lys	Leu	Asp	Ile	
129				405					410				415				
131	caa	cca	tat	gat	att	aat	caa	agg	ttg	caa	gat	aca	gga	ggg	tta	att	1296
132	Gln	Pro	Tyr	Asp	Ile	Asn	Gln	Arg	Leu	Gln	Asp	Thr	Gly	Gly	Leu	Ile	

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135	gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat	1344		
136	Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp			
137	435 440 445			
139	att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg	1392		
140	Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu			
141	450 455 460			
143	tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca	1440		
144	Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr			
145	465 470 475 480			
147	gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att	1488		
148	Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile			
149	485 490 495			
151	aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att	1536		
152	Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile			
153	500 505 510			
155	tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat	1584		
156	Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp			
157	515 520 525			
159	aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca	1632		
160	Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala			
161	530 535 540			
163	gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg	1680		
164	Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu			
165	545 550 555 560			
167	gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata	1728		
168	Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile			
169	565 570 575			
171	agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att	1776		
172	Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile			
173	580 585 590			
175	caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg	1824		
176	Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly			
177	595 600 605			
179	tta cca aaa tat aca aag ctt att aca ttc aac gtg cat aat aga tat	1872		
180	Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr			
181	610 615 620			
183	gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa	1920		
184	Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys			
185	625 630 635 640			
187	aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt	1968		
188	Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val			
189	645 650 655			
191	gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata	2016		
192	Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile			
193	660 665 670			
195	gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca	2064		
196	Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser			
197	675 680 685			

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203 tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa      2160
204 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu
205 705      710      715      720
207 ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac      2208
208 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn
209      725      730      735
211 caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag      2256
212 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys
213      740      745      750
215 gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa      2304
216 Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu
217      755      760      765
219 ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa      2352
220 Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu
221      770      775      780
223 cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac      2400
224 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn
225 785      790      795      800
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232 <210> SEQ ID NO: 2
233 <211> LENGTH: 809
234 <212> TYPE: PRT
235 <213> ORGANISM: Bacillus anthracis
237 <400> SEQUENCE: 2
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244      20      25      30
247 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu
248      35      40      45
251 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr
252      50      55      60
255 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
256 65      70      75      80
259 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
260      85      90      95
263 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly
264      100      105      110
267 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu
268      115      120      125
271 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
272      130      135      140
275 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro
276 145      150      155      160

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279 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys
280                      165                      170                      175
283 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile
284                      180                      185                      190
287 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
288                      195                      200                      205
291 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr
292                      210                      215                      220
295 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu
296 225                      230                      235                      240
299 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
300                      245                      250                      255
303 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu
304                      260                      265                      270
307 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser
308                      275                      280                      285
311 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
312                      290                      295                      300
315 Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
316 305                      310                      315                      320
319 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys
320                      325                      330                      335
323 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu
324                      340                      345                      350
327 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
328                      355                      360                      365
331 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu
332                      370                      375                      380
335 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro
336 385                      390                      395                      400
339 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile
340                      405                      410                      415
343 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile
344                      420                      425                      430
347 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp
348                      435                      440                      445
351 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu
352                      450                      455                      460
355 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr
356 465                      470                      475                      480
359 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile
360                      485                      490                      495
363 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile
364                      500                      505                      510
367 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
368                      515                      520                      525
371 Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala
372                      530                      535                      540
375 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu

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VERIFICATION SUMMARY

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